

Entry name	CLPP_ECOLI
Primary accession number	P19245
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 16, November 1990
Sequence was last modified in	Release 16, November 1990
Annotations were last modified in	Release 41, February 2003
Name and origin of the protein	
Protein name	ATP-dependent Clp protease proteolytic subunit
Synonyms	EC <u>3.4.21.92</u> Endopeptidase Clp Caseinolytic protease Protease Ti Heat shock protein F21.5
Gene name	CLPP or LOPP or <u>B0437</u> or <u>C0553</u> or <u>Z0542</u> or <u>ECS0491</u> or <u>SF0382</u>
From	<u>Escherichia coli</u> [TaxID: <u>562</u>] <u>Escherichia coli O6</u> [TaxID: <u>217992</u>] <u>Escherichia coli O157:H7</u> [TaxID: <u>83334</u>] <u>Shigella flexneri</u> [TaxID: <u>623</u>]
Taxonomy	Bacteria; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Enterobacteriales</u> ; <u>Enterobacteriaceae</u> ; <u>Escherichia</u> .
References	
[1]	SEQUENCE FROM NUCLEIC ACID. SPECIES=E.coli; MEDLINE=90324245; PubMed=2197275; [<u>NCBI</u> , <u>ExPASy</u> , <u>EBI</u> , <u>Israel</u> , <u>Japan</u>] <u>Maurizi M.R.</u> , <u>Clark W.P.</u> , <u>Katayama Y.</u> , <u>Rudikoff S.</u> , <u>Pumphrey J.</u> , <u>Bowers B.</u> , <u>Gottesman S.</u> ; "Sequence and structure of Clp P, the proteolytic component of the

	ATP-dependent Clp protease of Escherichia coli."; <u>J. Biol. Chem. 265:12536-12545(1990).</u>
[2]	SEQUENCE FROM NUCLEIC ACID. SPECIES =E.coli; STRAIN =K12 / MG1655; MEDLINE=97426617; PubMed=9278503; [<u>NCBI</u> , <u>ExPASy</u> , <u>EBI</u> , <u>Israel</u> , <u>Japan</u>] <u>Blattner F.R.</u> , <u>Plunkett G. III</u> , <u>Bloch C.A.</u> , <u>Perna N.T.</u> , <u>Burland V.</u> , <u>Riley M.</u> , <u>Collado-Vides J.</u> , <u>Glasner J.D.</u> , <u>Rode C.K.</u> , <u>Mayhew G.F.</u> , <u>Gregor J.</u> , <u>Davis</u> <u>N.W.</u> , <u>Kirkpatrick H.A.</u> , <u>Goeden M.A.</u> , <u>Rose D.J.</u> , <u>Mau B.</u> , <u>Shao Y.</u> ; "The complete genome sequence of Escherichia coli K-12."; <u>Science 277:1453-1474(1997).</u>
[3]	SEQUENCE FROM NUCLEIC ACID. SPECIES =E.coli; <u>Roberts D.</u> , <u>Allen E.</u> , <u>Araujo R.</u> , <u>Aparicio A.</u> , <u>Chung E.</u> , <u>Davis K.</u> , <u>Duncan M.</u> , <u>Federspiel N.</u> , <u>Hyman R.</u> , <u>Kalman S.</u> , <u>Komp C.</u> , <u>Kurdi O.</u> , <u>Lew H.</u> , <u>Lin D.</u> , <u>Namath A.</u> , <u>Oefner P.</u> , <u>Schramm S.</u> , <u>Davis R.W.</u> ; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
[4]	SEQUENCE FROM NUCLEIC ACID. SPECIES =E.coli; STRAIN =O6:H1 / CFT073 / ATCC 700928; MEDLINE=22388234; PubMed=12471157; [<u>NCBI</u> , <u>ExPASy</u> , <u>EBI</u> , <u>Israel</u> , <u>Japan</u>] <u>Welch R.A.</u> , <u>Burland V.</u> , <u>Plunkett G. III</u> , <u>Redford P.</u> , <u>Roesch P.</u> , <u>Rasko D.</u> , <u>Buckles E.L.</u> , <u>Liou S.-R.</u> , <u>Boutin A.</u> , <u>Hackett J.</u> , <u>Stroud D.</u> , <u>Mayhew G.F.</u> , <u>Rose D.J.</u> , <u>Zhou S.</u> , <u>Schwartz D.C.</u> , <u>Perna N.T.</u> , <u>Mobley H.L.T.</u> , <u>Donnenberg</u> <u>M.S.</u> , <u>Blattner F.R.</u> ; "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli."; <u>Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).</u>
[5]	SEQUENCE FROM NUCLEIC ACID. SPECIES =E.coli; STRAIN =O157:H7 / EDL933 / ATCC 700927; MEDLINE=21074935; PubMed=11206551; [<u>NCBI</u> , <u>ExPASy</u> , <u>EBI</u> , <u>Israel</u> , <u>Japan</u>]

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7."; *Nature* 409:529-533(2001).

[6] SEQUENCE FROM NUCLEIC ACID.

SPECIES=*E.coli*;

STRAIN=O157:H7 / RIMD 0509952;

MEDLINE=21156231; **PubMed**=11258796; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic comparison with a laboratory strain K-12."; *DNA Res.* 8:11-22(2001).

[7] SEQUENCE FROM NUCLEIC ACID.

SPECIES=*S.flexneri*;

STRAIN=301 / Serotype 2a;

MEDLINE=22272406; **PubMed**=12384590; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Yu J.;

"Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity through comparison with genomes of *Escherichia coli* K12 and O157."; *Nucleic Acids Res.* 30:4432-4441(2002).

[8] IDENTIFICATION AS A HEAT SHOCK PROTEIN.

SPECIES=*E.coli*;

MEDLINE=91008981; **PubMed**=2211522; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

	<p><u>Kroh H.E., Simon L.D.;</u> "The ClpP component of Clp protease is the sigma 32-dependent heat shock protein F21.5"; <u>J. Bacteriol. 172:6026-6034(1990).</u></p>
[9]	<p>CHARACTERIZATION. SPECIES=E.coli; MEDLINE=94012667; PubMed=8407953; [<u>NCBI</u>, <u>ExPASy</u>, <u>EBI</u>, <u>Israel</u>, <u>Japan</u>] <u>Arribas J., Castano J.G.;</u> "A comparative study of the chymotrypsin-like activity of the rat liver multicatalytic proteinase and the ClpP from Escherichia coli."; <u>J. Biol. Chem. 268:21165-21171(1993).</u></p>
[10]	<p>X-RAY CRYSTALLOGRAPHY. SPECIES=E.coli; MEDLINE=96428678; PubMed=8831780; [<u>NCBI</u>, <u>ExPASy</u>, <u>EBI</u>, <u>Israel</u>, <u>Japan</u>] <u>Shin D.H., Lee C.S., Chung C.H., Suh S.W.;</u> "Molecular symmetry of the ClpP component of the ATP-dependent Clp protease, an Escherichia coli homolog of 20 S proteasome."; <u>J. Mol. Biol. 262:71-76(1996).</u></p>
[11]	<p>X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 25-207. SPECIES=E.coli; MEDLINE=98050920; PubMed=9390554; [<u>NCBI</u>, <u>ExPASy</u>, <u>EBI</u>, <u>Israel</u>, <u>Japan</u>] <u>Wang J., Hartling J.A., Flanagan J.M.;</u> "The structure of ClpP at 2.3-A resolution suggests a model for ATP-dependent proteolysis."; <u>Cell 91:447-456(1997).</u></p>

Comments

FUNCTION: Cleaves peptides in various proteins in a process that requires ATP hydrolysis. Has a chymotrypsin-like activity. Plays a major role in the degradation of misfolded proteins. May play the role of a master protease which is attracted to different substrates by different specificity factors such as clpA or clpX.

CATALYTIC ACTIVITY: Hydrolysis of proteins to small peptides in the presence of ATP and magnesium. Alpha-casein is the usual test substrate. In the absence of ATP, only oligopeptides shorter than five residues are cleaved (such as succinyl-Leu-Tyr-|-NHMEC; and Leu-Tyr-Leu-|-Tyr-Trp, in which the cleavage of the -Tyr-|-Leu- and -Tyr-|-Trp- bond also occurs).

SUBUNIT: 14 CLPP SUBUNITS ASSEMBLE INTO A DISK-LIKE STRUCTURE WITH A CENTRAL CAVITY, RESEMBLING THE STRUCTURE OF EUKARYOTIC PROTEASOMES. IN THE PRESENCE OF ATP, CLPA OR CLPX SUBUNITS INTERACT WITH THE CLPP STRUCTURE TO FORM A 750 kDa COMPLEX THAT EXHIBITS ATP-DEPENDENT PROTEOLYTIC ACTIVITY.

SUBCELLULAR LOCATION: Cytoplasmic.

INDUCTION: By heat shock.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S14.

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Cross-references

EMBL	J05534; AAA23588.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE000150; AAC73540.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	U82664; AAB40193.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE016756; AAN79031.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE005223; AAG54787.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
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PIR	B36575; B36575.
PDB	1TYF; 17-JUN-98. [ExPASy / RCSB]
MEROPS	S14.001 ; -.
SWISS-2DPAGE	P19245 ; COLI.
ECO2DBASE	F021.5 ; 6TH EDITION.
EcoGene	EG10158 ; clpP.
EcoCyc	EG10158 ; clpP.
CMR	P19245 ; B0437.
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Pfam	PF00574 ; CLP_protease; 1.
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TIGRFAMs	TIGR00493 ; clpP; 1.
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ProtoNet	P19245 .

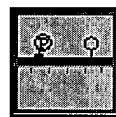
ProtoMap	<u>P19245.</u>
PRESAGE	<u>P19245.</u>
DIP	<u>P19245.</u>
ModBase	<u>P19245.</u>

Keywords

Hydrolase; Serine protease; Heat shock; 3D-structure; Complete proteome.

Features

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ACT_SITE	<u>136</u>	<u>136</u>		<i>PROBABLE.</i>
TURN	<u>29</u>	<u>32</u>	4	
HELIX	<u>33</u>	<u>39</u>	7	
TURN	<u>40</u>	<u>41</u>	2	
STRAND	<u>42</u>	<u>46</u>	5	
STRAND	<u>49</u>	<u>49</u>	1	
HELIX	<u>51</u>	<u>67</u>	17	
STRAND	<u>73</u>	<u>79</u>	7	
STRAND	<u>82</u>	<u>82</u>	1	
HELIX	<u>84</u>	<u>96</u>	13	
STRAND	<u>101</u>	<u>110</u>	10	
TURN	<u>111</u>	<u>111</u>	1	
HELIX	<u>112</u>	<u>118</u>	7	
TURN	<u>119</u>	<u>119</u>	1	
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STRAND	<u>125</u>	<u>127</u>	3	
TURN	<u>129</u>	<u>130</u>	2	
STRAND	<u>132</u>	<u>135</u>	4	
STRAND	<u>139</u>	<u>141</u>	3	
STRAND	<u>144</u>	<u>145</u>	2	
HELIX	<u>146</u>	<u>171</u>	26	
HELIX	<u>175</u>	<u>182</u>	8	
STRAND	<u>186</u>	<u>189</u>	4	



Feature table viewer

HELIX	<u>190</u>	<u>196</u>	7
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Sequence information

Length: **207** Molecular weight: **23186 Da** CRC64: **A7843D036C8CB3C2** [This is a checksum on the sequence]

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ID ECCLPPA standard; DNA; PRO; 1236 BP.
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 AC J05534;
 XX
 SV J05534.1
 XX
 DT 28-JUN-1990 (Rel. 24, Created)
 DT 04-MAR-2000 (Rel. 63, Last updated, Version 4)
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 DE Escherichia coli ATP-dependent clp protease proteolytic component (clpP)
 DE gene, complete cds.
 XX
 KW ATP-dependant protease.
 XX
 OS Escherichia coli
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
 OC Escherichia.
 XX
 RN [1]
 RP 1-1236
 RX MEDLINE; 90324245.
 RA Maurizi M.R., Clark W.P., Katayama Y., Rudikoff S., Pumphrey J., Bowers B.,
 RA Gottesman S.;
 RT "Sequence and structure of ClpP, the proteolytic component of the
 RT ATP-dependent Clp protease of Escherichia coli";
 RL J. Biol. Chem. 265:12536-12545(1990).
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 DR GOA; P19245; P19245.
 DR GOA; P22257; P22257.
 DR SWISS-PROT; P19245; CLPP_ECOLI.
 DR SWISS-PROT; P22257; TIG_ECOLI.
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 CC Draft entry and computer-readable sequence for [1] kindly submitted
 CC by S.Gottesman, 23-APR-1990.
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General information about the entry

Entry name	CLPP_YEREN
Primary accession number	Q60107
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 35, November 1997
Sequence was last modified in	Release 35, November 1997
Annotations were last modified in	Release 41, February 2003

Name and origin of the protein

Protein name	ATP-dependent Clp protease proteolytic subunit
Synonyms	EC <u>3.4.21.92</u> Endopeptidase Clp
Gene name	CLPP
From	<u>Yersinia enterocolitica</u> [TaxID: <u>630</u>]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Enterobacteriales</u> ; <u>Enterobacteriaceae</u> ; <u>Yersinia</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=8081C / Serotype O:8;
MEDLINE=98043541; **PubMed**=9383193; [NCBI, ExpASY, EBI, Israel, Japan]
Pederson K.J., Carlson S., Pierson D.E.;
 "The ClpP protein, a subunit of the Clp protease, modulates ail gene expression in *Yersinia enterocolitica*.";
 Mol. Microbiol. 26:99-107(1997).

Comments

FUNCTION: Cleaves peptides in various proteins in a process that requires ATP hydrolysis. Has a chymotrypsin-like activity. Plays a major role in the degradation of misfolded proteins (*By similarity*).

CATALYTIC ACTIVITY: Hydrolysis of proteins to small peptides in the presence of ATP and magnesium. Alpha-casein is the usual test substrate. In the absence of ATP, only oligopeptides shorter than five residues are

cleaved (such as succinyl-Leu-Tyr-|-NHMEC; and Leu-Tyr-Leu-|-Tyr-Trp, in which the cleavage of the -Tyr-|-Leu- and -Tyr-|-Trp- bond also occurs).

SUBCELLULAR LOCATION: Cytoplasmic (*By similarity*).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S14.

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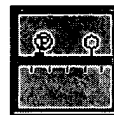
Cross-references

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HSSP	P19245; 1TYF. [HSSP ENTRY / PDB]
MEROPS	S14.001; -.
HAMAP	MF_00444; -; 1.
InterPro	IPR001907; CLP_protease. Graphical view of domain structure.
Pfam	PF00574; CLP_protease; 1.
PRINTS	PR00127; CLPPROTEASEP.
TIGRFAMs	TIGR00493; clpP; 1.
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ProtoMap	Q60107 .
PRESAGE	Q60107 .
DIP	Q60107 .
ModBase	Q60107 .
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Keywords

Hydrolase; Serine protease.**Features**

Key	From	To	Length	Description
ACT_SITE	111	111		BY SIMILARITY.
ACT_SITE	136	136		BY SIMILARITY.


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Sequence information

Length: 207 AA	Molecular weight: 23256 Da	CRC64: 865E0F6DB3DA07A1 [This is a checksum on the sequence]
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10	20	30	40	50	60
MSYSGERDQF	APNMALVPMV	VEQTSRGERS	YDIFSRLLEKE	RIIFLTGQVE	DHMANLITAQ
70	80	90	100	110	120
MLFLEAENPE	KDIFLYINSP	GGVITAGMSI	YDTMQFIKPD	VSTICMGQAC	SMGAFLLTAG
130	140	150	160	170	180
AKGKRFLCPN	SRVMIHQPLG	GFQGGATDIE	IHAKEILKVK	SRMNELMAKH	TGKSLEEIER
190	200				
DTERDRFLSA	DEAVEYGLVD	SVFTRRD			

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